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SEQUENCE LISTING

<110> Bander, Neil H.

<120> TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

<130> Lois M. Kwasigroch: BZL 242/024

<140> US 09/357,704
<141> 1999-07-20

<150> US 08/838,682
<151> 1997-04-09

<150> US 60/016,976
<151> 1996-05-06

<150> US 60/022,125
<151> 1996-07-18

<160> 21

<170> PatentIn version 3.0

<210> 1
<211> 391
<212> DNA
<213> Mus sp.

<400> 1
tctcctgtca ggaactgcag gtgtcctctc tgaggtccag ctgcaacagt ctggacctga 60

actggtgaag cctgggactt cagtgaggat atcctgcaag acttctggat acacattcac 120

tgaatatacc atacactggg tgaagcagag ccatggaaag agccttgagt ggattggaaa 180

catcaatcct aacaatggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt 240

gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga 300

ttctgcagtc tattattgtg cagctggttg gaactttgac tactggggcc aaggcaccac 360

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<210> 2
<211> 391
<212> DNA
<213> Mus sp.

<400> 2
gggtgtcgtt ttggctgagg agactgtgag agtggtgcct tggccccagt agtcaaagtt 60

ccaaccagct gcacaataat agactgcaga atcctcagat gttaggctgc ggagctccat 120

gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt 180

gtaggtggta ccaccattgt taggattgat gtttccaatc cactcaaggc tctttccatg 240

gctctgcttc acccagtgta tggtatattc agtgaatgtg tatccagaag tcttgcagga 300

tatcctcact gaagtcccag gcttcaccag ttcaggtcca gactgttgca gctggacctc 360

agagaggaca cctgcagttc ctagcaggag a 391

<210> 3
<211> 123
<212> PRT
<213> Mus sp.

<400> 3

Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val
1 5 10 15

Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp
20 25 30

Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro
35 40 45

Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
50 55 60

Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
65 70 75 80

Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
85 90 95

Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His
100 105 110

His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
115 120

<210> 4
<211> 130
<212> PRT
<213> Mus sp.

<400> 4

Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln
1 5 10 15

Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys
20 25 30

Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
35 40 45

Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
50 55 60

Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
65 70 75 80

Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
85 90 95

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
115 120 125

Thr Pro
130

<210> 5
<211> 125
<212> PRT
<213> Mus sp.

<400> 5

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
1 5 10 15

Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
115 120 125

<210> 6
<211> 345
<212> DNA
<213> Mus sp.

<400> 6
gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctgggacttc agtgaggata 60

tcctgcaaga cttctggata cacattcact gaatatacca tacactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggaaac atcaatccta acaatggtgg taccacctac 180

aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac 240

atggagctcc gcagcctaac atctgaggat tctgcagtct attattgtgc agctggttgg 300

aactttgact actggggcca aggcaccact ctcacagtct cctca 345

<210> 7
<211> 345

<212> DNA
<213> Mus sp.

<400> 7
tgaggagact gtgagagtgg tgccttggcc ccagtagtca aagttccaac cagctgcaca 60

ataatagact gcagaatcct cagatgttag gctgcggagc tccatgtagg ctgtactgga 120

ggacttgtct acagtcaatg tggccttgtc ctcgaacttc tgattgtagg tggtaccacc 180

attgttagga ttgatgtttc caatccactc aaggctcttt ccatggctct gcttcaccca 240

gtgtatggta tattcagtga atgtgtatcc agaagtcttg caggatatcc tcactgaagt 300

cccaggcttc accagttcag gtccagactg ttgcagctgg acctc 345

<210> 8
<211> 115
<212> PRT
<213> Mus sp.

<400> 8

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 9
<211> 363
<212> DNA
<213> Mus sp.

<400> 9
ttatatggag ctgatgggaa cattgtaatg acccaatctc ccaaatccat gtccatgtca 60

gtaggagaga gggtcacctt gacctgcaag gccagtgaga atgtggttac ttatgtttcc 120

tggtatcaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg 180

tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc 240

atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat 300

ccgtacacgt tcggaggggg gaccaagctg gaaataaaac gggctgatgc tgcaccaact 360

gta 363

<210> 10
<211> 363
<212> DNA
<213> Mus sp.

<400> 10
tacagttggt gcagcatcag cccgttttat ttccagcttg gtcccccctc cgaacgtgta 60

cggatagctg taaccctgtc cacagtgata atctgcaagg tcttcagcct gcacactgct 120

gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggaccccagt 180

gtaccggttg gatgccccgt atatcagcag tttaggagac tgctctggtt tctgttgata 240

ccaggaaaca taagtaacca cattctcact ggccttgcag gtcaaggtga ccctctctcc 300

tactgacatg gacatggatt tgggagattg ggtcattaca atgttcccat cagctccata 360

taa 363

<210> 11
<211> 121
<212> PRT
<213> Mus sp.

<400> 11

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser
1 5 10 15

Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser
20 25 30

Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
85 90 95

Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Ala Asp Ala Ala Pro Thr Val
115 120

<210> 12

<211> 114
<212> PRT
<213> Mus sp.

<400> 12

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30

Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45

Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60

Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80

Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95

Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110

Leu Tyr

<210> 13
<211> 116
<212> PRT
<213> Mus sp.

<400> 13

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
1 5 10 15

Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
20 25 30

Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
35 40 45

Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
50 55 60

Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
65 70 75 80

Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
85 90 95

Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
100 105 110

Cys Thr Asn Cys
115

<210> 14
<211> 321
<212> DNA
<213> Mus sp.

<400> 14
aacattgtaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 15
<211> 321
<212> DNA
<213> Mus sp.

<400> 15
ttttatttcc agcttggtcc cccctccgaa cgtgtacgga tagctgtaac cctgtccaca 60

gtgataatct gcaaggtctt cagcctgcac actgctgatg gtcagagtga aatctgttgc 120

agatccactg cctgtgaagc gatcggggac cccagtgtac cggttggatg ccccgtatat 180

cagcagttta ggagactgct ctggtttctg ttgataccag gaaacataag taaccacatt 240

ctcactggcc ttgcaggtca aggtgaccct ctctcctact gacatggaca tggatttggg 300

agattgggtc attacaatgt t 321

<210> 16
<211> 107
<212> PRT
<213> Mus sp.

<400> 16

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr

85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 17
<211> 321
<212> DNA
<213> Mus sp.

<400> 17
gacattgtga tgacccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc 60

atcatctgta aggccagtca agatgtgggt actgctgtag actggtatca acagaaacca 120

ggacaatctc ctaaactact gatttattgg gcatccactc ggcacactgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagac ttcactctca ccattactaa tgttcagtct 240

gaagacttgg cagattattt ctgtcagcaa tataacagct atcctctcac gttcggtgct 300

gggaccatgc tggacctgaa a 321

<210> 18
<211> 321
<212> DNA
<213> Mus sp.

<400> 18
tttcaggtcc agcatggtcc cagcaccgaa cgtgagagga tagctgttat attgctgaca 60

gaaataatct gccaagtctt cagactgaac attagtaatg gtgagagtga agtctgtccc 120

agatccactg cctgtgaagc gatcagggac tccagtgtgc cgagtggatg cccaataaat 180

cagtagttta ggagattgtc ctggtttctg ttgataccag tctacagcag tacccacatc 240

ttgactggcc ttacagatga tgctgaccct gtctcctact gatgtggaca tgaatttgtg 300

agactgggtc atcacaatgt c 321

<210> 19
<211> 107
<212> PRT
<213> Mus sp.

<400> 19

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
100 105

<210> 20
<211> 125
<212> PRT
<213> Mus sp.

<400> 20

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Asn Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp
35 40 45

Ile Gly Asp Ile Asn Pro Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Tyr Tyr Ser Ser Ser Tyr Met Ala Tyr Tyr Ala Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 21
<211> 109
<212> PRT
<213> Mus sp.

<400> 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu

65 70 75 80

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
85 90 95

Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105